

SEQUENCE LISTING

<110> Joshua Z. Levin
Ken Phillips
Greg Budziszewski
Fred Meins
Zhenya Glazov

<120> Methods of Controlling Gene Expression

<130> PB/5-31481A

<140>

<141>

<160> 34

<170> PatentIn Ver. 2.1

<210> 1

<211> 942

<212> DNA

<213> Arabidopsis thaliana

<400> 1

```
atgtcatcgt caaattggat cgacgacgct ttacagagg aagagcttct cgctatcgac 60
gccatcgaag cttcctacaa tttctcccg tcttcttctt cttcttcctc tgctgctccg 120
accgtacaag ctacaacctc cgtccatggc cagaggagg atccaaatca aatccccaat 180
aatatccgtc gccaatgcc tcgttccatc acttcttcta catcttataa acgatttcct 240
ctctcccggt gccgagctag gaattttcca gcaatgaggt ttggtggtag gattttgtat 300
agcaagactg ctactgaggt tgataagcga gcaatgcagc ttattaaagt tcttgatacc 360
aagagagatg aatctggaat agcttttgtt ggcttgata ttgagtggag accaagtttt 420
agaaaagggt ttctcccggt gaagggtgag actgtccaga tatgtgtaga tagtaattat 480
tgtgatgtta tgcatatttt tcattctggt atccctcaaa gtctccaaca tcttattgaa 540
gattcaacac ttgtaaagggt aggtattgga attgatggtg actctgtgaa gcttttccat 600
gactatggag ttagtatcaa agatgttgag gatctttcag atttagccaa ccaaaaaatt 660
ggtggagata aaaaatgggg ccttgctca ctaactgaga cacttggttg caaagagctc 720
ctgaagccaa acagaatcag gcttggaac tgggagtttt atcctctgtc aaagcagcag 780
ttacaatacg cagcaacgga tgcttatgct tcatggcatc ttacaagggt aacaacaacg 840
aaaaaccatc ttctcacact caacgacctt gaagcaaaaa tctcacatcg ttctaattat 900
aatactgtta cttgtcgaaa acctggaggt tatcttcggt ga 942
```

<210> 2

<211> 313

<212> PRT

<213> Arabidopsis thaliana

<400> 2

Met Ser Ser Ser Asn Trp Ile Asp Asp Ala Phe Thr Glu Glu Glu Leu
1 5 10 15

Leu Ala Ile Asp Ala Ile Glu Ala Ser Tyr Asn Phe Ser Arg Ser Ser
20 25 30

Ser Ser Ser Ser Ser Ala Ala Pro Thr Val Gln Ala Thr Thr Ser Val
35 40 45

His Gly His Glu Glu Asp Pro Asn Gln Ile Pro Asn Asn Ile Arg Arg
 50 55 60
 Gln Leu Pro Arg Ser Ile Thr Ser Ser Thr Ser Tyr Lys Arg Phe Pro
 65 70 75 80
 Leu Ser Arg Cys Arg Ala Arg Asn Phe Pro Ala Met Arg Phe Gly Gly
 85 90 95
 Arg Ile Leu Tyr Ser Lys Thr Ala Thr Glu Val Asp Lys Arg Ala Met
 100 105 110
 Gln Leu Ile Lys Val Leu Asp Thr Lys Arg Asp Glu Ser Gly Ile Ala
 115 120 125
 Phe Val Gly Leu Asp Ile Glu Trp Arg Pro Ser Phe Arg Lys Gly Val
 130 135 140
 Leu Pro Gly Lys Val Ala Thr Val Gln Ile Cys Val Asp Ser Asn Tyr
 145 150 155 160
 Cys Asp Val Met His Ile Phe His Ser Gly Ile Pro Gln Ser Leu Gln
 165 170 175
 His Leu Ile Glu Asp Ser Thr Leu Val Lys Val Gly Ile Gly Ile Asp
 180 185 190
 Gly Asp Ser Val Lys Leu Phe His Asp Tyr Gly Val Ser Ile Lys Asp
 195 200 205
 Val Glu Asp Leu Ser Asp Leu Ala Asn Gln Lys Ile Gly Gly Asp Lys
 210 215 220
 Lys Trp Gly Leu Ala Ser Leu Thr Glu Thr Leu Val Cys Lys Glu Leu
 225 230 235 240
 Leu Lys Pro Asn Arg Ile Arg Leu Gly Asn Trp Glu Phe Tyr Pro Leu
 245 250 255
 Ser Lys Gln Gln Leu Gln Tyr Ala Ala Thr Asp Ala Tyr Ala Ser Trp
 260 265 270
 His Leu Tyr Lys Val Thr Thr Thr Lys Asn His Leu Leu Thr Leu Asn
 275 280 285
 Asp Leu Glu Ala Lys Ile Ser His Arg Ser Asn Tyr Asn Thr Val Thr
 290 295 300
 Cys Arg Lys Pro Gly Gly Tyr Leu Arg
 305 310

<210> 3
 <211> 1929
 <212> DNA
 <213> Arabidopsis thaliana

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

<210> 4

<212> PRT

<213> Arabidopsis thaliana

Met Arg Phe Asp Asp Pro Met Asp Glu Phe Lys Arg Asn Arg Lys Met
1 5 10 15

Glu Glu Asp Ser Lys Lys Val Ile Asp Val Lys Val Ala Glu Ser Asp
20 25 30

Lys Gly Phe Ala Lys Phe Gly Lys Ala Glu Val Pro Phe His Ile Pro
35 40 45

Thr Leu Thr Lys Pro Gln Glu Glu Tyr Lys Ile Leu Val Asp Asn Ala
50 55 60

Asn Asn Pro Phe Glu His Val Leu Leu Glu Lys Ser Glu Asp Gly Leu
65 70 75 80

Arg Arg Leu Leu Lys Ser Lys Leu Pro Tyr Leu Glu Arg Asn Phe Asp
 385 390 395 400
 Ala Val Ile Ser Val Ile Arg Arg Ser Met Gln Asn Ala Ala Ala Phe
 405 410 415
 Glu Pro Val Val Gln Ser Leu Lys Asp Arg Arg Pro Glu Thr Val Val
 420 425 430
 Glu Met Asn Ile Glu Pro Lys Ile Glu Lys Thr Asp Thr Gly Ala Ser
 435 440 445
 Ala Ser Ser Leu Ser Leu Glu Lys Val Cys Val Asp Asp Ser Lys Lys
 450 455 460
 Gln Ser Ser Gly Phe Gly Val Leu Pro Leu Lys Arg Lys Leu Glu Ser
 465 470 475 480
 Asp Lys Thr Val Val Glu Lys Asn Ile Glu Pro Lys Ile Glu Lys Thr
 485 490 495
 Gly Thr Glu Ala Ser Ala Ser Ser Leu Ser Ser Lys Lys Val Cys Val
 500 505 510
 Asp Asp Ser Lys Lys Gln Ser Ser Gly Phe Gly Val Leu Leu Ser Lys
 515 520 525
 Arg Lys Phe Glu Ser Asp Asn Lys Lys Leu Gln Val Lys Glu Glu Val
 530 535 540
 Lys Val Ser Lys Ser Lys Pro Asp Lys Val Ile Ile Val Val Asp Asp
 545 550 555 560
 Asp Asp Asp Asp Asp Asp Asp Glu Ser Tyr Glu Gln Ser Thr Lys Ala
 565 570 575
 Ala Asp Ala Leu Asp Arg Val Ser Glu Thr Pro Ser Lys Gly Ser Pro
 580 585 590
 Ser Leu Thr Gln Lys Pro Lys Thr Cys Asn Thr Glu Val Ile Val Leu
 595 600 605
 Asp Asp Asp Asp Asp Ser Glu Ser Arg Glu Asp Glu Asp Met Arg Arg
 610 615 620
 Arg Ser Glu Lys His Arg Arg Phe Met Asn Met Lys Arg Gly Phe Leu
 625 630 635 640
 Asn Ile

<210> 5
 <211> 714
 <212> DNA
 <213> Arabidopsis thaliana

<400> 5

atgaatttgc attttgattt ttggtgtttt atatttgaaa ctaatgcaga gaaaccttcg 60
aatggtcatc catatgaaac tgagatcact gttttgttag agaatcctca gattgagttt 120
ggatttttga gaggagagtg ttcattggaa atgagtgatt catatgtgtg ggttgagaca 180
gagtcgcagt taaaggaact tgcagaaata ttagcaaaaag aacaagtttt tgcggttgac 240
actgagcagc atagtttgcg gtcgtttcctt ggtttccactg ctctaattca gatttctaca 300
catgaggaag acttttttgtt ggacacaatt gcgttacatg atgtaatgag tattcttcgt 360
cctgttttct ctgatacctaa tatttgtaag gtgtttcacg gggctgacaa cgatgttatc 420
tggcttcaaa gagacttcca tatatatgtt gttaatatgt ttgatactgc caaggcatgt 480
gaagtgttgt caaagcctca acgatcactg gcatacttac ttgagacagt atgtggagtg 540
gctactaaca aattgctgca gcgtgaagat tggagacagc gtcctctgtc cgaagagatg 600
gtgcgatatg ctagaacaga tgcacactat ctgctttata ttgcagatag tttgacaact 660
gaactcaaac aattagccac tggtaggcac ctttgctatg gagaaacatt ttag 714

<210> 6

<211> 237

<212> PRT

<213> Arabidopsis thaliana

<400> 6

Met Asn Leu His Phe Asp Phe Trp Cys Phe Ile Phe Glu Thr Asn Ala
1 5 10 15
Glu Lys Pro Ser Asn Gly His Pro Tyr Glu Thr Glu Ile Thr Val Leu
20 25 30
Leu Glu Asn Pro Gln Ile Glu Phe Gly Phe Leu Arg Gly Glu Cys Ser
35 40 45
Leu Glu Met Ser Asp Ser Tyr Val Trp Val Glu Thr Glu Ser Gln Leu
50 55 60
Lys Glu Leu Ala Glu Ile Leu Ala Lys Glu Gln Val Phe Ala Val Asp
65 70 75 80
Thr Glu Gln His Ser Leu Arg Ser Phe Leu Gly Phe Thr Ala Leu Ile
85 90 95
Gln Ile Ser Thr His Glu Glu Asp Phe Leu Val Asp Thr Ile Ala Leu
100 105 110
His Asp Val Met Ser Ile Leu Arg Pro Val Phe Ser Asp Pro Asn Ile
115 120 125
Cys Lys Val Phe His Gly Ala Asp Asn Asp Val Ile Trp Leu Gln Arg
130 135 140
Asp Phe His Ile Tyr Val Val Asn Met Phe Asp Thr Ala Lys Ala Cys
145 150 155 160
Glu Val Leu Ser Lys Pro Gln Arg Ser Leu Ala Tyr Leu Leu Glu Thr
165 170 175
Val Cys Gly Val Ala Thr Asn Lys Leu Leu Gln Arg Glu Asp Trp Arg
180 185 190

Ile Ser Tyr Glu Glu Lys Glu Glu Val Arg Val Leu Met Arg Gln Asp
100 105 110

Pro Lys Phe Trp Thr Tyr Arg Pro Met Thr Glu Leu Met Ile Arg Ala
115 120 125

Ala Ala Asp Asp Val Arg Phe Leu Leu Tyr Leu Tyr His Lys Met Met
130 135 140

Gly Lys Leu Asn Gln Arg Ser Leu Trp His Leu Ala Val Arg Gly Ala
145 150 155 160

Leu Tyr Cys Arg Cys Leu Cys Cys Met Asn Asp Ala Asp Phe Ala Asp
165 170 175

Trp Pro Thr Val Pro Pro Ile Pro Val Phe Leu Val Lys Val Val Tyr
180 185 190

Ala Val Glu Thr Lys Lys Lys Arg Arg Val Thr Leu Ala Ser Ile Gly
195 200 205

Leu Leu Ile Val Val Gly Leu Leu Asn Val Ala Asp Asn Leu Lys Ser
210 215 220

Glu Asp Gln Cys Leu Glu Glu Glu Ile Leu Ser Val Leu Asp Val Pro
225 230 235 240

Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu
245 250 255

Ala Ile Lys Glu Ala Cys Asn Ala Glu Ile Leu Ile Gly Gly Ala Lys
260 265 270

Gly Pro Pro Asp Lys Val Ser Leu Ile Pro
275 280

<210> 9

<211> 720

<212> DNA

<213> Arabidopsis thaliana

<400> 9

atggctagga tcagaagaag aatccaaaag cgccatatcc acgaaaaccg ctacatcgat 60
ttctttggag aacgtttgat cgtcacggtc actcatacta cctcaaccat ccgccgttgg 120
attcatagca tccgtttctt cagccgtctt cgctcctcac accctctcgt tgttggactc 180
gacgtccaat ggacaccggg tggttccgat cctccaccgg atattctcca actatgtgtt 240
ggtaaccgct gtctcatcat ccagttgtct cactgtaaac gcattcctga ggtccttcga 300
agtttcttgg aagatgagac aatcactttt gtcggcgtct ggaacagcca agaccagggc 360
aagctcgaag gattccgcca tcagttggag atatggagac ttctagacat aaggcactat 420
ctgcctacga ggctcctcaa tagttcgttt gagaagattg tagaggagtg tttgggggtac 480
aagggagtga ggaaagataa ggagatatgt atgagtaatt ggggtgctcg tagcctttcc 540
catgatcaga ttgttcaggc gtcagatgat gtctatgttt gctgcaagct cggtgttaag 600
gaatgtatct ggaaagagcg ctccaatgtt aaagaacgta tctggaaaga gagctcgaat 660
gttaaggaac atatctggaa agagagctcg aaactttatt ttgttggggg atgttttctga 720

<210> 10
 <211> 239
 <212> PRT
 <213> Arabidopsis thaliana

<400> 10
 Met Ala Arg Ile Arg Arg Arg Ile Gln Lys Arg His Ile His Glu Asn
 1 5 10 15
 Arg Tyr Ile Asp Phe Phe Gly Glu Arg Leu Ile Val Thr Val Thr His
 20 25 30
 Thr Thr Ser Thr Ile Arg Arg Trp Ile His Ser Ile Arg Phe Phe Ser
 35 40 45
 Arg Leu Arg Ser Ser His Pro Leu Val Val Gly Leu Asp Val Gln Trp
 50 55 60
 Thr Pro Gly Gly Ser Asp Pro Pro Pro Asp Ile Leu Gln Leu Cys Val
 65 70 75 80
 Gly Asn Arg Cys Leu Ile Ile Gln Leu Ser His Cys Lys Arg Ile Pro
 85 90 95
 Glu Val Leu Arg Ser Phe Leu Glu Asp Glu Thr Ile Thr Phe Val Gly
 100 105 110
 Val Trp Asn Ser Gln Asp Gln Gly Lys Leu Glu Arg Phe Arg His Gln
 115 120 125
 Leu Glu Ile Trp Arg Leu Leu Asp Ile Arg His Tyr Leu Pro Thr Arg
 130 135 140
 Leu Leu Asn Ser Ser Phe Glu Lys Ile Val Glu Glu Cys Leu Gly Tyr
 145 150 155 160
 Lys Gly Val Arg Lys Asp Lys Glu Ile Cys Met Ser Asn Trp Gly Ala
 165 170 175
 Arg Ser Leu Ser His Asp Gln Ile Val Gln Ala Ser Asp Asp Val Tyr
 180 185 190
 Val Cys Cys Lys Leu Gly Val Lys Glu Cys Ile Trp Lys Glu Arg Ser
 195 200 205
 Asn Val Lys Glu Arg Ile Trp Lys Glu Ser Ser Asn Val Lys Glu His
 210 215 220
 Ile Trp Lys Glu Ser Ser Lys Leu Tyr Phe Val Gly Val Cys Phe
 225 230 235

<210> 11
 <211> 654
 <212> DNA
 <213> Arabidopsis thaliana

09896186-062901

<400> 11

```
atgaagagag gtatcaaaca tctatgtttc aatggcttca cgggctactc atcacttcat 60
catcattatc atgaacacca cgtcgacttc tttggagaac gtttgatcgt cacagtcact 120
catactccct cagtgatagc tcgatggatc cacagtatcc gcttcgtcag ccgtcttcgc 180
ttatcacacc ctctagttgt cggacttggc gttcaatgga caccctgtgg ttccgatacct 240
ccaccggata ttctccaact atgtgttggg actcgctgtc tcatcattca gttgtctcac 300
tgtaagtacg tccccgacgt ccttagaagt ttcttggaag atcagacaat cacttttgtc 360
ggcgtatgga acagccaaga caaggacaag ctcgagagat tccaccatca gttggatata 420
tggagacttg tccacataag gcactatctc catccgttgc tcttgagtag ctcgtttgag 480
acgattgtga aggtgtatct ggggcatgaa ggagtgacga aagataagga gttatgtatg 540
agtaattggg gtgctcgtag cctctctcat gatcagatag tacaagcgtc acatgatgtc 600
tatgtttgct gcaagctcgg tgtaaaggaa cgtctctgga aaatgggagc ttaa 654
```

<210> 12

<211> 217

<212> PRT

<213> Arabidopsis thaliana

<400> 12

```
Met Lys Arg Gly Ile Lys His Leu Cys Phe Asn Gly Phe Thr Gly Tyr
  1             5             10             15

Ser Ser Leu His His His Tyr His Glu His His Val Asp Phe Phe Gly
      20             25             30

Glu Arg Leu Ile Val Thr Val Thr His Thr Pro Ser Val Ile Arg Arg
      35             40             45

Trp Ile His Ser Ile Arg Phe Val Ser Arg Leu Arg Leu Ser His Pro
      50             55             60

Leu Val Val Gly Leu Gly Val Gln Trp Thr Pro Arg Gly Ser Asp Pro
      65             70             75             80

Pro Pro Asp Ile Leu Gln Leu Cys Val Gly Thr Arg Cys Leu Ile Ile
      85             90             95

Gln Leu Ser His Cys Lys Tyr Val Pro Asp Val Leu Arg Ser Phe Leu
      100            105            110

Glu Asp Gln Thr Ile Thr Phe Val Gly Val Trp Asn Ser Gln Asp Lys
      115            120            125

Asp Lys Leu Glu Arg Phe His His Gln Leu Asp Ile Trp Arg Leu Val
      130            135            140

His Ile Arg His Tyr Leu His Pro Leu Leu Leu Ser Ser Ser Phe Glu
      145            150            155            160

Thr Ile Val Lys Val Tyr Leu Gly His Glu Gly Val Thr Lys Asp Lys
      165            170            175

Glu Leu Cys Met Ser Asn Trp Gly Ala Arg Ser Leu Ser His Asp Gln
      180            185            190

Ile Val Gln Ala Ser His Asp Val Tyr Val Cys Cys Lys Leu Gly Val
```

195

200

205

Lys Glu Arg Leu Trp Lys Met Gly Ala
 210 215

<210> 13

<211> 261

<212> DNA

<213> Arabidopsis thaliana

<400> 13

atgatcaagt cgatcgagag ctttattgct cgttatgttt tccaagctac attatacaca 60
 atctggtgcg aacgaaatgg cagaaggcat ggagagagag aggccgaacc agccgctctt 120
 ctaataaaat tgattgataa gcaagccatc tttcctcaat cagagcaact gatgatctac 180
 gctatgacaa gagcctccaa atctggtttg catcgagtgg ttgaaatcaa accatctata 240
 gttcatgtgt ttaaccttta a 261

<210> 14

<211> 86

<212> PRT

<213> Arabidopsis thaliana

<400> 14

Met Ile Lys Ser Ile Glu Ser Phe Ile Ala Arg Tyr Val Phe Gln Ala
 1 5 10 15

Thr Leu Tyr Thr Ile Trp Cys Glu Arg Asn Gly Arg Arg His Gly Glu
 20 25 30

Arg Glu Ala Glu Pro Ala Ala Leu Leu Ile Lys Leu Ile Asp Lys Gln
 35 40 45

Ala Ile Phe Pro Gln Ser Glu Gln Leu Met Ile Tyr Ala Met Thr Arg
 50 55 60

Ala Ser Lys Ser Gly Leu His Arg Val Val Glu Ile Lys Pro Ser Ile
 65 70 75 80

Val His Val Phe Asn Leu
 85

<210> 15

<211> 2733

<212> DNA

<213> C. elegans

<400> 15

atggaagaag aaccgtacaa aagaaagcta acgaaagccg agaaaaaggc aaaatatcga 60
 acagactacg ccgaaccgtt gaagtcacgc cggaaggttc tgaaagcaat tatgaatgga 120
 cccgagtctg agcgggagag aaaagtctga gccaaaaatc gagaattttt caacgaggac 180
 tatagatcag gagtcaacat ctacggaatg gctgtggata tgatgaaagc gatgccggat 240
 agaggaaaaa catcgggaca aagtttggcg gtttggtatc tggaggattt tggagtttgg 300
 ttaaaagagt cgggacagga gacggagctc agacagaaat atctgactgg aactattcaa 360
 ataaacgcct tagatgtgtg cacaattgga caaaagcagc ttctcagtga aatcttcgat 420

```

atcaccaaag agaaattcac tgaggacatt acacagttgc tagatgctgc catcaagaaa 480
caagacttct ccgttgctgc agatatggct attcagtaca atcttctacg ggatcatcat 540
ttcgaacatc ttgttcttcc attaatgcta tctggcaaag atcaaacggc ttataaattg 600
ataagtaaca atgagaggat gcaacagcag cttgtagagt tttttgatcg aatgggttga 660
atctcagtgg ttgccgttga agagatgctg aaaccctaca aggaaaccaa aattatgacg 720
attcctatgg agaaattgac gggaaaaacg ttggacaaac tcatttcgac gattatcaac 780
aaaaatactc acgaatacaa cttctccagg gaattgtcga agttcgccaa aaaccactca 840
cagaatggga atctgaaggc attgaagttt aatatcagtg aacgatacga gaagggaaaa 900
tccgatgaca actatttcca gcatatggtt gaaactttta ccaaagccga agatgttcgt 960
gaacctattt tgttttactt gtggagctca aatgacaccg agaaacaaat agatgccatc 1020
tgcttttgcta tctacttagg aatcgctagt tccagcagct atcaactgcc gaatggtatg 1080
agggacttct ttcgacaacc tgattcgaag ctacagagaag caaaagaact tctagtga 1140
agaaaaacac tgcaagttcc tctaaatggc gaacaattat tcgtatttga gaatgagcga 1200
agaactcaaa tccacatggt gaaaactgaa tctgagatga attacttatg ttccgagatc 1260
aaatcactaa gcgacgagcc agcacctgtt tacgttggat tcgattctga gtggaaaccg 1320
tcgaatctta cagctgttca tgactcgaaa attgctatca tacaattgtt cttcaaaaat 1380
tgtgtatggc ttgtggattg cgtagaatta gaaaaggcaa atatggcaga tgactggtgg 1440
caaaagttcg catctcgatt gttcggagat tctcctgtaa aagtcgtagg atttgatatg 1500
aggaacgatc tggatgcaat ggctacaatc ccagcactga agtcatccat gaagatagaa 1560
gataccaaaa atgcattcga tctgaagcga ttagcagaga atgtttgcga tatcgacatg 1620
gaaatttttag agctgcaaaa gaagactttc aaattggcag atttgacaca ttatctactg 1680
ggattggagc tcgacaaaac tgaacaatgc agtaactggc aatgtcgtcc tctgcgaaaa 1740
aaacaaattg tgtacgcagc attggacgca gttgtcgtgg tggaaacatt caagaaaatc 1800
ttgtcgattg tagaggagaa aaacaaggac gcagatatcg agaagattgt cagagaatca 1860
aatgtaatgg ctccgaaaaa agacaaagga cacaaatcgt accgcaagct gaaaactatt 1920
ccatggcttg agctctacga tatcttgca agccatcgta atcctacgag atcaccacag 1980
cgaccacacg acattaaagt tattgttgac acaatgctga ttggatttgg aaagaatctg 2040
aggagagttg gaattgatgt tattcttcca aaagacgtga gcgacttccg aaagtacctg 2100
aaggaaattg aacgagttgg cggcgagcat ctacgtcata taatcacagt gccatcgaaa 2160
agttacgaag ccttgaaaaa ggattatgat aattatacaa ttgcaattcc ggaactcaat 2220
aacatgtctc ccgtagatca gcttattgag tttttcgacc tgttcaacgt agatattcgt 2280
ccggaagacg tatatcctcg atgcactgaa tgcaattctc ggcttcaa ataaattccc 2340
ggaccagttt tacatttctt gcaccaatac tgtgtcatcc atgtgcaaaa tgtttatcgt 2400
gcggatatga gcgaatttcc actggaagaa tgggtggaatc gtatgcttca tatcaatcca 2460
gacgactacg acggagtaaa agtggaatg tcgcgaccat ctccaacaag caagtggatc 2520
gtggcaactg ttcccacagg atgcctacat attacgcgac aaactgcact tcacaccaat 2580
ctgccagatg gaattgaagt tcgaatccac aaagtgcctg atgacgagtt caagcgtcga 2640
aatctcagct tctatgtgtg tggagaatgc ggtacggtgg cttgtgatgg tcgtggcaat 2700
caagcgtcgg agagcaccag ccaggaatgt tga 2733

```

<210> 16
 <211> 910
 <212> PRT
 <213> C. elegans

<400> 16
 Met Glu Glu Glu Pro Tyr Lys Arg Lys Leu Thr Lys Ala Glu Lys Lys
 1 5 10 15
 Ala Lys Tyr Arg Thr Asp Tyr Ala Glu Pro Leu Lys Ser Arg Arg Glu
 20 25 30
 Val Leu Lys Ala Ile Met Asn Gly Pro Glu Ser Glu Arg Glu Arg Lys
 35 40 45
 Val Arg Ala Lys Asn Arg Glu Phe Phe Asn Glu Asp Tyr Arg Ser Gly

09090185-062901

50					55					60					
Val	Asn	Ile	Tyr	Gly	Met	Ala	Val	Asp	Met	Met	Lys	Ala	Met	Pro	Asp
65					70					75					80
Arg	Gly	Lys	Thr	Ser	Gly	Gln	Ser	Leu	Ala	Val	Trp	Tyr	Leu	Glu	Asp
				85					90					95	
Phe	Gly	Val	Trp	Leu	Lys	Glu	Ser	Gly	Gln	Glu	Thr	Glu	Leu	Arg	Gln
			100					105					110		
Lys	Tyr	Leu	Thr	Gly	Thr	Ile	Gln	Ile	Asn	Ala	Leu	Asp	Val	Cys	Thr
		115					120					125			
Ile	Gly	Gln	Lys	Gln	Leu	Leu	Ser	Glu	Ile	Phe	Asp	Ile	Thr	Lys	Glu
	130					135					140				
Lys	Phe	Thr	Glu	Asp	Ile	Thr	Gln	Leu	Leu	Asp	Ala	Ala	Ile	Lys	Lys
145						150				155					160
Gln	Asp	Phe	Ser	Val	Ala	Ala	Asp	Met	Ala	Ile	Gln	Tyr	Asn	Leu	Leu
				165					170					175	
Arg	Asp	His	His	Phe	Glu	His	Leu	Val	Leu	Pro	Leu	Met	Leu	Ser	Gly
			180					185					190		
Lys	Asp	Gln	Thr	Ala	Tyr	Lys	Leu	Ile	Ser	Asn	Asn	Glu	Arg	Met	Gln
		195					200					205			
Gln	Gln	Leu	Val	Glu	Phe	Phe	Asp	Arg	Met	Val	Gly	Ile	Ser	Val	Val
	210					215					220				
Ala	Val	Glu	Glu	Met	Leu	Lys	Pro	Tyr	Lys	Glu	Thr	Lys	Ile	Met	Thr
225					230					235					240
Ile	Pro	Met	Glu	Lys	Leu	Thr	Gly	Lys	Thr	Leu	Asp	Lys	Leu	Ile	Ser
				245					250					255	
Thr	Ile	Ile	Asn	Lys	Asn	Thr	His	Glu	Tyr	Asn	Phe	Ser	Arg	Glu	Leu
			260					265					270		
Ser	Lys	Phe	Ala	Lys	Asn	His	Ser	Gln	Asn	Gly	Asn	Leu	Lys	Ala	Leu
		275					280					285			
Lys	Phe	Asn	Ile	Ser	Glu	Arg	Tyr	Glu	Lys	Gly	Lys	Ser	Asp	Asp	Asn
	290					295				300					
Tyr	Phe	Gln	His	Met	Val	Glu	Thr	Phe	Thr	Lys	Ala	Glu	Asp	Val	Arg
305					310					315					320
Glu	Pro	Ile	Leu	Phe	Tyr	Leu	Trp	Ser	Ser	Asn	Asp	Thr	Glu	Lys	Gln
				325					330					335	
Ile	Asp	Ala	Ile	Cys	Phe	Ala	Ile	Tyr	Leu	Gly	Ile	Ala	Ser	Ser	Ser
			340					345					350		
Ser	Tyr	Gln	Leu	Pro	Asn	Val	Met	Arg	Asp	Phe	Phe	Arg	Gln	Pro	Asp

008896186 062901

355					360					365					
Ser	Lys	Leu	Arg	Glu	Ala	Lys	Glu	Leu	Leu	Val	Arg	Arg	Lys	Thr	Leu
	370					375					380				
Gln	Val	Pro	Leu	Asn	Gly	Glu	Gln	Leu	Phe	Val	Phe	Glu	Asn	Glu	Arg
	385					390					395				400
Arg	Thr	Gln	Ile	His	Met	Val	Lys	Thr	Glu	Ser	Glu	Met	Asn	Tyr	Leu
				405					410					415	
Cys	Ser	Glu	Ile	Lys	Ser	Leu	Ser	Asp	Glu	Pro	Ala	Pro	Val	Tyr	Val
			420					425					430		
Gly	Phe	Asp	Ser	Glu	Trp	Lys	Pro	Ser	Asn	Leu	Thr	Ala	Val	His	Asp
		435					440					445			
Ser	Lys	Ile	Ala	Ile	Ile	Gln	Leu	Phe	Phe	Lys	Asn	Cys	Val	Trp	Leu
	450					455					460				
Val	Asp	Cys	Val	Glu	Leu	Glu	Lys	Ala	Asn	Met	Ala	Asp	Asp	Trp	Trp
	465					470					475				480
Gln	Lys	Phe	Ala	Ser	Arg	Leu	Phe	Gly	Asp	Ser	Pro	Val	Lys	Val	Val
				485					490					495	
Gly	Phe	Asp	Met	Arg	Asn	Asp	Leu	Asp	Ala	Met	Ala	Thr	Ile	Pro	Ala
			500					505					510		
Leu	Lys	Ser	Ser	Met	Lys	Ile	Glu	Asp	Thr	Lys	Asn	Ala	Phe	Asp	Leu
		515					520					525			
Lys	Arg	Leu	Ala	Glu	Asn	Val	Cys	Asp	Ile	Asp	Met	Glu	Ile	Leu	Glu
	530					535					540				
Leu	Pro	Lys	Lys	Thr	Phe	Lys	Leu	Ala	Asp	Leu	Thr	His	Tyr	Leu	Leu
	545					550					555				560
Gly	Leu	Glu	Leu	Asp	Lys	Thr	Glu	Gln	Cys	Ser	Asn	Trp	Gln	Cys	Arg
				565					570					575	
Pro	Leu	Arg	Lys	Lys	Gln	Ile	Val	Tyr	Ala	Ala	Leu	Asp	Ala	Val	Val
			580					585					590		
Val	Val	Glu	Thr	Phe	Lys	Lys	Ile	Leu	Ser	Ile	Val	Glu	Glu	Lys	Asn
		595					600					605			
Lys	Asp	Ala	Asp	Ile	Glu	Lys	Ile	Val	Arg	Glu	Ser	Asn	Val	Met	Ala
	610					615					620				
Pro	Lys	Lys	Asp	Lys	Gly	His	Lys	Ser	Tyr	Arg	Lys	Leu	Lys	Thr	Ile
	625					630					635				640
Pro	Trp	Leu	Glu	Leu	Tyr	Asp	Ile	Leu	Arg	Ser	His	Arg	Asn	Pro	Thr
				645					650					655	
Arg	Ser	Pro	Gln	Arg	Pro	His	Asp	Ile	Lys	Val	Ile	Val	Asp	Thr	Met

09896185-062901

660					665					670						
Leu	Ile	Gly	Phe	Gly	Lys	Asn	Leu	Arg	Arg	Val	Gly	Ile	Asp	Val	Ile	
675					680					685						
Leu	Pro	Lys	Asp	Val	Ser	Asp	Phe	Arg	Lys	Tyr	Leu	Lys	Glu	Ile	Glu	
690					695					700						
Arg	Val	Gly	Gly	Glu	His	Leu	Arg	His	Ile	Ile	Thr	Val	Pro	Ser	Lys	
705					710					715					720	
Ser	Tyr	Glu	Ala	Leu	Lys	Met	Asp	Tyr	Asp	Asn	Tyr	Thr	Ile	Ala	Ile	
725					730					735						
Pro	Glu	Leu	Asn	Asn	Met	Ser	Pro	Val	Asp	Gln	Leu	Ile	Glu	Phe	Phe	
740					745					750						
Asp	Leu	Phe	Asn	Val	Asp	Ile	Arg	Pro	Glu	Asp	Val	Tyr	Pro	Arg	Cys	
755					760					765						
Thr	Glu	Cys	Asn	Ser	Arg	Leu	Gln	Ile	Lys	Phe	Pro	Gly	Pro	Val	Leu	
770					775					780						
His	Phe	Leu	His	Gln	Tyr	Cys	Val	Ile	His	Val	Gln	Asn	Val	Tyr	Arg	
785					790					795					800	
Ala	Asp	Met	Ser	Glu	Phe	Pro	Leu	Glu	Glu	Trp	Trp	Asn	Arg	Met	Leu	
805					810					815						
His	Ile	Asn	Pro	Asp	Asp	Tyr	Asp	Gly	Val	Lys	Val	Glu	Met	Ser	Arg	
820					825					830						
Pro	Ser	Pro	Thr	Ser	Lys	Trp	Ile	Val	Ala	Thr	Val	Pro	Thr	Gly	Cys	
835					840					845						
Leu	His	Ile	Thr	Arg	Gln	Thr	Ala	Leu	His	Thr	Asn	Leu	Pro	Asp	Gly	
850					855					860						
Ile	Glu	Val	Arg	Ile	His	Lys	Val	Pro	Asp	Asp	Glu	Phe	Lys	Arg	Arg	
865					870					875					880	
Asn	Leu	Ser	Phe	Tyr	Val	Cys	Gly	Glu	Cys	Gly	Thr	Val	Ala	Cys	Asp	
885					890					895						
Gly	Arg	Gly	Asn	Gln	Ala	Ser	Glu	Ser	Thr	Ser	Gln	Glu	Cys			
900					905					910						

<210> 17

<211> 4299

<212> DNA

<213> Homo sapiens

<400> 17

atgagtga aaatttgga aacaactgca cagcagcgga aatgtcctga atggatgaat 60
gtgcagaata aaagatgtgc tgtagaagaa agaaaggcat gtgttcggaa gagtggtttt 120
gaagatgacc tccccttctt agaattcact ggatccattg tgtatagtta cgatgctagt 180

gattgctctt	tcctgtcaga	agatattagc	atgagtctat	cagatgggga	tgtgggtggga	240
tttgacatgg	agtggccacc	attatacaat	agagggaaac	ttggcaaagt	tgcactaatt	300
cagttgtgtg	tttctgagag	caaatgttac	ttgttccacg	tttcttccat	gtcagttttt	360
ccccagggat	taaaaatggt	gcttgaaaat	aaagcagtta	aaaaggcagg	tgttaggaatt	420
gaaggagatc	agtggaaaact	tctacgtgac	tttgatatca	aattgaagaa	ttttgtggag	480
ttgacagatg	ttgccaataa	aaagctgaaa	tgtacagaga	cctggagcct	taacagctctg	540
gttaaaccac	tcttaggtaa	acagctcctg	aaagacaagt	ctatccgctg	tagcaatttg	600
agtaaatttc	ctctcactga	ggaccagaaa	ctgtatgcag	ccactgatgc	ttatgctggt	660
tttattatct	accgaaatct	agagattttg	gatgatactg	tgcaaagggt	tgctataaat	720
aaagaggaag	aaatcctact	tagcgacatg	aacaaacagt	tgacttcaat	ctctgaggaa	780
gtgatggatc	tggctaagca	tcttctcat	gctttcagta	aattggaaaa	cccacggagg	840
gtttctatct	tactaaagga	tatttcagaa	aatctatatt	cactgaggag	gatgataatt	900
gggtctacta	acattgagac	tgaactgagg	cccgaataa	atttaaactt	attatccttt	960
gaagattcaa	ctactggggg	agtacaacag	aaacaaatta	gagaacatga	agtttttaatt	1020
cacgttgaag	atgaaacatg	ggacccaaca	cttgatcatt	tagctaaaca	tgatggagaa	1080
gatgtacttg	gaaataaagt	ggaacgaaaa	gaagatggat	ttgaagatgg	agtagaagac	1140
aacaaattga	aagagaatat	ggaaagagct	tgtttgatgt	cgtagatat	tacagaacat	1200
gaactccaaa	ttttggaaca	gcagtctcag	gaagaatatc	ttagtgatat	tgcttataaa	1260
tctactgagc	atttatctcc	caatgataat	gaaaacgata	cgctctatgt	aattgagagt	1320
gatgaagatt	tagaaatgga	gatgcttaag	catttatctc	ccaatgataa	tgaaaacgat	1380
acgtcctatg	taattgagag	tgatgaagat	ttagaaatgg	agatgcttaa	gtcttttagaa	1440
aacctcaata	gtggcacggg	agaaccaact	cattctaaat	gcttaaaaaa	ggaaagaaat	1500
ctgggtcttc	ctactaaaga	agaagaagaa	gatgatgaaa	atgaagctaa	tgaaggggaa	1560
gaagatgatg	ataaggactt	tttgtggcca	gcacccaatg	aagagcaagt	tacttgcctc	1620
aagatgtact	ttggccattc	cagtttttaa	ccagttcagt	ggaaagtgat	tcattcagta	1680
ttagaagaaa	gaagagataa	tgttgctgtc	atggcaactg	gatatggaaa	gagtttgtgc	1740
ttccagtatc	cacctgttta	tgtaggcaag	attggccttg	ttatctctcc	ccttattttct	1800
ctgatggaag	accaagtgtc	acagcttaaa	atgtccaaca	tcccagcttg	cttccttgga	1860
tcagcacagt	cagaaaatgt	tctaacagat	attaaattag	gtaaataaccg	gattgtatac	1920
gtaactccag	aatactgttc	aggtaacatg	ggcctgtccc	agcaacttga	ggctgatatt	1980
ggatcacgcg	tcattgctgt	ggatgaggct	cactgtattt	ctgagtgggg	gcatgatttt	2040
agggattcat	tcagggaagt	gggtccctta	aagacgacac	tgccaatggg	tccaatcggt	2100
gcacttactg	ctactgcaag	ttcttcaatc	cgggaagaca	ttgtacgttg	cttaaatctg	2160
agaaatcctc	agatcacctg	tactggtttt	gatcgacca	acctgtattt	agaagttagg	2220
cgaaaaacag	ggaatatcct	tcaggatctg	cagccatttc	ttgtcaaaac	aagttcccac	2280
tgggaatttg	aaggtccaac	aatcatctac	tgtccttcta	gaaaaatgac	acaacaagtt	2340
acaggtgaac	ttaggaaact	taatctatcc	tgtggaacat	accatgcggg	catgagtttt	2400
agcacaagga	aagacattca	tcataggttt	gtaagagatg	aaattcagtg	tgtcatagct	2460
accatagctt	ttggaatggg	cattaataaa	gctgacattc	gccaagtcac	tcattacggg	2520
gctcctaagg	acatggaatc	atattatcag	gagattggta	gagctggctg	tgatggactt	2580
caaagttctt	gtcacgtcct	ctgggctcct	gcagacatta	acttaaatag	gcaccttctt	2640
actgagatac	gtaatgagaa	gtttcgatta	tacaaattaa	agatgatggc	aaagatggaa	2700
aaatatcttc	attctagcag	atgtaggaga	caaatcatct	tgtctcattt	tgaggacaaa	2760
caagtacaaa	aagcctcctt	gggaattatg	ggaactgaaa	aatgctgtga	taattgcagg	2820
tccagatttg	atcattgcta	ttccatggat	gactcagagg	atacatcctg	ggactttggg	2880
ccacaagcat	ttaagctttt	gtctgctgtg	gacatcttag	gcgaaaaatt	tggaattggg	2940
cttccaatct	tatttctccg	aggatcta	tctcagcgtc	ttgccgatca	atatcgcagg	3000
cacagtttat	ttggcactgg	caaggatcaa	acagagagtt	ggtggaaggc	tttttcccgt	3060
cagctgatca	ctgagggatt	cttggtagaa	gtttctcggt	ataacaaatt	tatgaagatt	3120
tgcgccctta	cgaaaaaggg	tagaaattgg	cttcataaag	ctaatacaga	atctcagagc	3180
ctcatccttc	aagctaattg	agaattgtgt	ccaaagaagt	ttcttctgcc	tagttcgaaa	3240
actgtatctt	cgggcaccaa	agagcattgt	tataatcaag	taccagttga	attaagtaca	3300
gagaagaagt	ctaacttgga	gaagttatat	tcttataaac	catgtgataa	gatttcttct	3360
gggagtaaca	tttctaaaaa	aagtatcatg	gtacagtcac	cagaaaaagc	ttacagttcc	3420
tcacagcctg	ttatttcggc	acaagagcag	gagactcaga	ttgtgttata	tggaatttg	3480
gtagaagcta	ggcagaaaca	tgccaataaa	atggatgttc	ccccagctat	tctggcaaca	3540
aacaagatac	tggtggatat	ggccaaaatg	agaccaacta	cggttgaaaa	cgtaaaaagg	3600

```

attgatggtg tttctgaagg caaagctgcc atgttggccc ctctgttggga agtcatcaaa 3660
catttctgcc aaacaaatag tggtcagaca gacctctttt caagtacaaa acctcaagaa 3720
gaacagaaga cgagtctggt agcaaaaaat aaaatatgca cactttcaca gtctatggcc 3780
atcacatact ctttattcca agaaaagaag atgcctttga agagcatagc tgagagcagg 3840
attctgcctc tcatgacaat tggcatgcac ttatcccaag cggtgaaaagc tggctgcccc 3900
cttgatttgg agcgagcagg cctgactcca gaggttcaga agattattgc tgatgttatc 3960
cgaaaccctc ccgtcaactc agatatgagt aaaattagcc taatcagaat gttagtctcct 4020
gaaaacattg acacgtacct tatccacatg gcaattgaga tccttaaaca tggctcctgac 4080
agcggacttc aaccttcatt tgatgtcaac aaaaggagat gttttcccggt ttctgaagag 4140
atctgttcaa gttctaagag aagcaaggaa gaagtaggca tcaatactga gacttcattc 4200
gcagagagaa agagacgatt acctgtgtgg tttgccaaag gaagtgatac cagcaagaaa 4260
ttaatggaca aaacgaaaaa gggaggtctt tttagttaa 4299

```

<210> 18
 <211> 1432
 <212> PRT
 <213> Homo sapiens

<400> 18

Met	Ser	Glu	Lys	Lys	Leu	Glu	Thr	Thr	Ala	Gln	Gln	Arg	Lys	Cys	Pro
1				5					10					15	
Glu	Trp	Met	Asn	Val	Gln	Asn	Lys	Arg	Cys	Ala	Val	Glu	Glu	Arg	Lys
			20					25					30		
Ala	Cys	Val	Arg	Lys	Ser	Val	Phe	Glu	Asp	Asp	Leu	Pro	Phe	Leu	Glu
		35					40					45			
Phe	Thr	Gly	Ser	Ile	Val	Tyr	Ser	Tyr	Asp	Ala	Ser	Asp	Cys	Ser	Phe
	50					55					60				
Leu	Ser	Glu	Asp	Ile	Ser	Met	Ser	Leu	Ser	Asp	Gly	Asp	Val	Val	Gly
65					70					75					80
Phe	Asp	Met	Glu	Trp	Pro	Pro	Leu	Tyr	Asn	Arg	Gly	Lys	Leu	Gly	Lys
				85					90					95	
Val	Ala	Leu	Ile	Gln	Leu	Cys	Val	Ser	Glu	Ser	Lys	Cys	Tyr	Leu	Phe
			100					105					110		
His	Val	Ser	Ser	Met	Ser	Val	Phe	Pro	Gln	Gly	Leu	Lys	Met	Leu	Leu
		115					120					125			
Glu	Asn	Lys	Ala	Val	Lys	Lys	Ala	Gly	Val	Gly	Ile	Glu	Gly	Asp	Gln
	130					135					140				
Trp	Lys	Leu	Leu	Arg	Asp	Phe	Asp	Ile	Lys	Leu	Lys	Asn	Phe	Val	Glu
145				150						155					160
Leu	Thr	Asp	Val	Ala	Asn	Lys	Lys	Leu	Lys	Cys	Thr	Glu	Thr	Trp	Ser
			165					170						175	
Leu	Asn	Ser	Leu	Val	Lys	His	Leu	Leu	Gly	Lys	Gln	Leu	Leu	Lys	Asp
		180					185						190		
Lys	Ser	Ile	Arg	Cys	Ser	Asn	Trp	Ser	Lys	Phe	Pro	Leu	Thr	Glu	Asp

	195					200					205				
Gln	Lys	Leu	Tyr	Ala	Ala	Thr	Asp	Ala	Tyr	Ala	Gly	Phe	Ile	Ile	Tyr
	210					215					220				
Arg	Asn	Leu	Glu	Ile	Leu	Asp	Asp	Thr	Val	Gln	Arg	Phe	Ala	Ile	Asn
225					230					235					240
Lys	Glu	Glu	Glu	Ile	Leu	Leu	Ser	Asp	Met	Asn	Lys	Gln	Leu	Thr	Ser
				245					250					255	
Ile	Ser	Glu	Glu	Val	Met	Asp	Leu	Ala	Lys	His	Leu	Pro	His	Ala	Phe
			260					265					270		
Ser	Lys	Leu	Glu	Asn	Pro	Arg	Arg	Val	Ser	Ile	Leu	Leu	Lys	Asp	Ile
		275					280					285			
Ser	Glu	Asn	Leu	Tyr	Ser	Leu	Arg	Arg	Met	Ile	Ile	Gly	Ser	Thr	Asn
	290					295					300				
Ile	Glu	Thr	Glu	Leu	Arg	Pro	Ser	Asn	Asn	Leu	Asn	Leu	Leu	Ser	Phe
305					310					315					320
Glu	Asp	Ser	Thr	Thr	Gly	Gly	Val	Gln	Gln	Lys	Gln	Ile	Arg	Glu	His
				325					330					335	
Glu	Val	Leu	Ile	His	Val	Glu	Asp	Glu	Thr	Trp	Asp	Pro	Thr	Leu	Asp
			340					345					350		
His	Leu	Ala	Lys	His	Asp	Gly	Glu	Asp	Val	Leu	Gly	Asn	Lys	Val	Glu
		355					360					365			
Arg	Lys	Glu	Asp	Gly	Phe	Glu	Asp	Gly	Val	Glu	Asp	Asn	Lys	Leu	Lys
	370					375					380				
Glu	Asn	Met	Glu	Arg	Ala	Cys	Leu	Met	Ser	Leu	Asp	Ile	Thr	Glu	His
385					390					395					400
Glu	Leu	Gln	Ile	Leu	Glu	Gln	Gln	Ser	Gln	Glu	Glu	Tyr	Leu	Ser	Asp
				405					410					415	
Ile	Ala	Tyr	Lys	Ser	Thr	Glu	His	Leu	Ser	Pro	Asn	Asp	Asn	Glu	Asn
			420					425					430		
Asp	Thr	Ser	Tyr	Val	Ile	Glu	Ser	Asp	Glu	Asp	Leu	Glu	Met	Glu	Met
		435					440					445			
Leu	Lys	His	Leu	Ser	Pro	Asn	Asp	Asn	Glu	Asn	Asp	Thr	Ser	Tyr	Val
	450					455					460				
Ile	Glu	Ser	Asp	Glu	Asp	Leu	Glu	Met	Glu	Met	Leu	Lys	Ser	Leu	Glu
465					470					475					480
Asn	Leu	Asn	Ser	Gly	Thr	Val	Glu	Pro	Thr	His	Ser	Lys	Cys	Leu	Lys
				485					490					495	
Met	Glu	Arg	Asn	Leu	Gly	Leu	Pro	Thr	Lys	Glu	Glu	Glu	Glu	Asp	Asp

500							505					510				
Glu	Asn	Glu	Ala	Asn	Glu	Gly	Glu	Glu	Asp	Asp	Asp	Lys	Asp	Phe	Leu	
		515						520						525		
Trp	Pro	Ala	Pro	Asn	Glu	Glu	Gln	Val	Thr	Cys	Leu	Lys	Met	Tyr	Phe	
		530						535						540		
Gly	His	Ser	Ser	Phe	Lys	Pro	Val	Gln	Trp	Lys	Val	Ile	His	Ser	Val	
		545						550						555		
Leu	Glu	Glu	Arg	Arg	Asp	Asn	Val	Ala	Val	Met	Ala	Thr	Gly	Tyr	Gly	
								565						570		
Lys	Ser	Leu	Cys	Phe	Gln	Tyr	Pro	Pro	Val	Tyr	Val	Gly	Lys	Ile	Gly	
								580						585		
Leu	Val	Ile	Ser	Pro	Leu	Ile	Ser	Leu	Met	Glu	Asp	Gln	Val	Leu	Gln	
		595						600						605		
Leu	Lys	Met	Ser	Asn	Ile	Pro	Ala	Cys	Phe	Leu	Gly	Ser	Ala	Gln	Ser	
		610						615						620		
Glu	Asn	Val	Leu	Thr	Asp	Ile	Lys	Leu	Gly	Lys	Tyr	Arg	Ile	Val	Tyr	
		625						630						635		
Val	Thr	Pro	Glu	Tyr	Cys	Ser	Gly	Asn	Met	Gly	Leu	Leu	Gln	Gln	Leu	
								645						650		
Glu	Ala	Asp	Ile	Gly	Ile	Thr	Leu	Ile	Ala	Val	Asp	Glu	Ala	His	Cys	
								660						665		
Ile	Ser	Glu	Trp	Gly	His	Asp	Phe	Arg	Asp	Ser	Phe	Arg	Lys	Leu	Gly	
		675						680						685		
Ser	Leu	Lys	Thr	Ala	Leu	Pro	Met	Val	Pro	Ile	Val	Ala	Leu	Thr	Ala	
		690						695						700		
Thr	Ala	Ser	Ser	Ser	Ile	Arg	Glu	Asp	Ile	Val	Arg	Cys	Leu	Asn	Leu	
		705						710						715		
Arg	Asn	Pro	Gln	Ile	Thr	Cys	Thr	Gly	Phe	Asp	Arg	Pro	Asn	Leu	Tyr	
								725						730		
Leu	Glu	Val	Arg	Arg	Lys	Thr	Gly	Asn	Ile	Leu	Gln	Asp	Leu	Gln	Pro	
								740						745		
Phe	Leu	Val	Lys	Thr	Ser	Ser	His	Trp	Glu	Phe	Glu	Gly	Pro	Thr	Ile	
		755						760						765		
Ile	Tyr	Cys	Pro	Ser	Arg	Lys	Met	Thr	Gln	Gln	Val	Thr	Gly	Glu	Leu	
		770						775						780		
Arg	Lys	Leu	Asn	Leu	Ser	Cys	Gly	Thr	Tyr	His	Ala	Gly	Met	Ser	Phe	
		785						790						795		
Ser	Thr	Arg	Lys	Asp	Ile	His	His	Arg	Phe	Val	Arg	Asp	Glu	Ile	Gln	

			805					810					815				
Cys	Val	Ile	Ala	Thr	Ile	Ala	Phe	Gly	Met	Gly	Ile	Asn	Lys	Ala	Asp		
			820					825					830				
Ile	Arg	Gln	Val	Ile	His	Tyr	Gly	Ala	Pro	Lys	Asp	Met	Glu	Ser	Tyr		
			835					840					845				
Tyr	Gln	Glu	Ile	Gly	Arg	Ala	Gly	Arg	Asp	Gly	Leu	Gln	Ser	Ser	Cys		
			850					855					860				
His	Val	Leu	Trp	Ala	Pro	Ala	Asp	Ile	Asn	Leu	Asn	Arg	His	Leu	Leu		
			865					870					875		880		
Thr	Glu	Ile	Arg	Asn	Glu	Lys	Phe	Arg	Leu	Tyr	Lys	Leu	Lys	Met	Met		
			885					890					895				
Ala	Lys	Met	Glu	Lys	Tyr	Leu	His	Ser	Ser	Arg	Cys	Arg	Arg	Gln	Ile		
			900					905					910				
Ile	Leu	Ser	His	Phe	Glu	Asp	Lys	Gln	Val	Gln	Lys	Ala	Ser	Leu	Gly		
			915					920					925				
Ile	Met	Gly	Thr	Glu	Lys	Cys	Cys	Asp	Asn	Cys	Arg	Ser	Arg	Leu	Asp		
			930					935					940				
His	Cys	Tyr	Ser	Met	Asp	Asp	Ser	Glu	Asp	Thr	Ser	Trp	Asp	Phe	Gly		
			945					950					955		960		
Pro	Gln	Ala	Phe	Lys	Leu	Leu	Ser	Ala	Val	Asp	Ile	Leu	Gly	Glu	Lys		
			965					970					975				
Phe	Gly	Ile	Gly	Leu	Pro	Ile	Leu	Phe	Leu	Arg	Gly	Ser	Asn	Ser	Gln		
			980					985					990				
Arg	Leu	Ala	Asp	Gln	Tyr	Arg	Arg	His	Ser	Leu	Phe	Gly	Thr	Gly	Lys		
			995					1000					1005				
Asp	Gln	Thr	Glu	Ser	Trp	Trp	Lys	Ala	Phe	Ser	Arg	Gln	Leu	Ile	Thr		
			1010					1015					1020				
Glu	Gly	Phe	Leu	Val	Glu	Val	Ser	Arg	Tyr	Asn	Lys	Phe	Met	Lys	Ile		
			1025					1030					1035		1040		
Cys	Ala	Leu	Thr	Lys	Lys	Gly	Arg	Asn	Trp	Leu	His	Lys	Ala	Asn	Thr		
			1045					1050					1055				
Glu	Ser	Gln	Ser	Leu	Ile	Leu	Gln	Ala	Asn	Glu	Glu	Leu	Cys	Pro	Lys		
			1060					1065					1070				
Lys	Phe	Leu	Leu	Pro	Ser	Ser	Lys	Thr	Val	Ser	Ser	Gly	Thr	Lys	Glu		
			1075					1080					1085				
His	Cys	Tyr	Asn	Gln	Val	Pro	Val	Glu	Leu	Ser	Thr	Glu	Lys	Lys	Ser		
			1090					1095					1100				
Asn	Leu	Glu	Lys	Leu	Tyr	Ser	Tyr	Lys	Pro	Cys	Asp	Lys	Ile	Ser	Ser		

106290-9879860

1105	1110	1115	1120
Gly Ser Asn Ile Ser Lys Lys Ser Ile Met Val Gln Ser Pro Glu Lys	1125	1130	1135
Ala Tyr Ser Ser Ser Gln Pro Val Ile Ser Ala Gln Glu Gln Glu Thr	1140	1145	1150
Gln Ile Val Leu Tyr Gly Lys Leu Val Glu Ala Arg Gln Lys His Ala	1155	1160	1165
Asn Lys Met Asp Val Pro Pro Ala Ile Leu Ala Thr Asn Lys Ile Leu	1170	1175	1180
Val Asp Met Ala Lys Met Arg Pro Thr Thr Val Glu Asn Val Lys Arg	1185	1190	1195
Ile Asp Gly Val Ser Glu Gly Lys Ala Ala Met Leu Ala Pro Leu Leu	1205	1210	1215
Glu Val Ile Lys His Phe Cys Gln Thr Asn Ser Val Gln Thr Asp Leu	1220	1225	1230
Phe Ser Ser Thr Lys Pro Gln Glu Glu Gln Lys Thr Ser Leu Val Ala	1235	1240	1245
Lys Asn Lys Ile Cys Thr Leu Ser Gln Ser Met Ala Ile Thr Tyr Ser	1250	1255	1260
Leu Phe Gln Glu Lys Lys Met Pro Leu Lys Ser Ile Ala Glu Ser Arg	1265	1270	1275
Ile Leu Pro Leu Met Thr Ile Gly Met His Leu Ser Gln Ala Val Lys	1285	1290	1295
Ala Gly Cys Pro Leu Asp Leu Glu Arg Ala Gly Leu Thr Pro Glu Val	1300	1305	1310
Gln Lys Ile Ile Ala Asp Val Ile Arg Asn Pro Pro Val Asn Ser Asp	1315	1320	1325
Met Ser Lys Ile Ser Leu Ile Arg Met Leu Val Pro Glu Asn Ile Asp	1330	1335	1340
Thr Tyr Leu Ile His Met Ala Ile Glu Ile Leu Lys His Gly Pro Asp	1345	1350	1355
Ser Gly Leu Gln Pro Ser Cys Asp Val Asn Lys Arg Arg Cys Phe Pro	1365	1370	1375
Gly Ser Glu Glu Ile Cys Ser Ser Ser Lys Arg Ser Lys Glu Glu Val	1380	1385	1390
Gly Ile Asn Thr Glu Thr Ser Ser Ala Glu Arg Lys Arg Arg Leu Pro	1395	1400	1405
Val Trp Phe Ala Lys Gly Ser Asp Thr Ser Lys Lys Leu Met Asp Lys			

1410 1415 1420
 Thr Lys Arg Gly Gly Leu Phe Ser
 1425 1430

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 19
 cgacatgatc tgatacatcg ttatgccatt 30

<210> 20
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 20
 cattttataa taacgctgcg gacatctac 29

<210> 21
 <211> 1041
 <212> DNA
 <213> Arabidopsis thaliana

<400> 21
 atgtttgagt ttttcgcttc aggaggaagg tcgccgacac aagaagctaa tgagccacca 60
 gttccgattt acattgtgac ggatccggtt caacttcctg ctgatttcct aaacccttct 120
 cctgaaaaga aattgggtat cggttttgac tgtgagggtg ttgacctctg ccgacatggg 180
 aaactttgta tcatgcagat tgcattctct aatgcaatat acttggttga tgtcatcgaa 240
 ggtggagagg tgattatgaa agcgtgtaag cctgcactcg agtctaatta catcacgaaa 300
 gttattcacg attgcaagcg tgacagttag gctctatact tccagtttgg gataagattg 360
 cacaatgttg tggacactca gattgcttat tctctgattg aagaacaaga agggcggagg 420
 agacctctag atgattacat atcgtttggt tcaactcctg ctgatccacg ttactgcggt 480
 atatcctatg aagagaaaaga agaagttcga gttctcatgc gccaggaccc aaagttttgg 540
 acatacaggc ctatgactga gtcctatgat cgcgcagctg ctgatgatgt ccgcttcctt 600
 ctgtatctct atcacaaaat gatgggaaag ctaaatcagc ggtcactatg gcatcttgca 660
 gttcgtggtg ctttgtactg tcggtgtctc tgctgcatga atgatgctga ttttgctgat 720
 tggccaaccg ttcctccaat tccagttttc ctcgttaagg tcgtatatgc tgtagagaca 780
 aagaaaaaaa gacgggtgac attagcttcg attgggttac tgattgtagt tggactttta 840
 aatgtggcag ataacctgaa gtcagaagat caatgtcttg aagaagagat cctgtcagtg 900
 cttgatgttc caccaggaaa gatgggacgt gtgattggaa ggaaaggagc atcgatcctc 960
 gccattaagg aagcttgcaa cgcggaaatt ctaattggag gggcaaaggg tccacctgat 1020
 aagggttagtc ttattccata g 1041

<210> 22
 <211> 346
 <212> PRT
 <213> Arabidopsis thaliana

<400> 22

Met	Phe	Glu	Phe	Phe	Ala	Ser	Gly	Gly	Arg	Ser	Pro	Thr	Gln	Glu	Ala	
1				5					10					15		
Asn	Glu	Pro	Pro	Val	Pro	Ile	Tyr	Ile	Val	Thr	Asp	Pro	Phe	Gln	Leu	
			20					25					30			
Pro	Ala	Asp	Phe	Leu	Asn	Pro	Ser	Pro	Glu	Lys	Lys	Leu	Val	Ile	Gly	
		35					40					45				
Phe	Asp	Cys	Glu	Gly	Val	Asp	Leu	Cys	Arg	His	Gly	Lys	Leu	Cys	Ile	
	50					55					60					
Met	Gln	Ile	Ala	Phe	Ser	Asn	Ala	Ile	Tyr	Leu	Val	Asp	Val	Ile	Glu	
65					70					75					80	
Gly	Gly	Glu	Val	Ile	Met	Lys	Ala	Cys	Lys	Pro	Ala	Leu	Glu	Ser	Asn	
				85					90					95		
Tyr	Ile	Thr	Lys	Val	Ile	His	Asp	Cys	Lys	Arg	Asp	Ser	Glu	Ala	Leu	
			100					105					110			
Tyr	Phe	Gln	Phe	Gly	Ile	Arg	Leu	His	Asn	Val	Val	Asp	Thr	Gln	Ile	
		115					120					125				
Ala	Tyr	Ser	Leu	Ile	Glu	Glu	Gln	Glu	Gly	Arg	Arg	Arg	Pro	Leu	Asp	
	130					135					140					
Asp	Tyr	Ile	Ser	Phe	Val	Ser	Leu	Leu	Ala	Asp	Pro	Arg	Tyr	Cys	Gly	
145					150					155					160	
Ile	Ser	Tyr	Glu	Glu	Lys	Glu	Glu	Val	Arg	Val	Leu	Met	Arg	Gln	Asp	
				165					170					175		
Pro	Lys	Phe	Trp	Thr	Tyr	Arg	Pro	Met	Thr	Glu	Leu	Met	Ile	Arg	Ala	
			180					185					190			
Ala	Ala	Asp	Asp	Val	Arg	Phe	Leu	Leu	Tyr	Leu	Tyr	His	Lys	Met	Met	
		195					200					205				
Gly	Lys	Leu	Asn	Gln	Arg	Ser	Leu	Trp	His	Leu	Ala	Val	Arg	Gly	Ala	
	210					215					220					
Leu	Tyr	Cys	Arg	Cys	Leu	Cys	Cys	Met	Asn	Asp	Ala	Asp	Phe	Ala	Asp	
225					230					235					240	
Trp	Pro	Thr	Val	Pro	Pro	Ile	Pro	Val	Phe	Leu	Val	Lys	Val	Val	Tyr	
				245					250					255		
Ala	Val	Glu	Thr	Lys	Lys	Lys	Arg	Arg	Val	Thr	Leu	Ala	Ser	Ile	Gly	
			260					265					270			

098961069601

Leu Leu Ile Val Val Gly Leu Leu Asn Val Ala Asp Asn Leu Lys Ser
 275 280 285

Glu Asp Gln Cys Leu Glu Glu Glu Ile Leu Ser Val Leu Asp Val Pro
 290 295 300

Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu
 305 310 315 320

Ala Ile Lys Glu Ala Cys Asn Ala Glu Ile Leu Ile Gly Gly Ala Lys
 325 330 335

Gly Pro Pro Asp Lys Val Ser Leu Ile Pro
 340 345

<210> 23
 <211> 1049
 <212> DNA
 <213> Arabidopsis thaliana

<400> 23
 accaaagcat taatttttat ttttttgttt cagtaaaaga aatgtcatcg tcaaattgga 60
 tcgacgacgc ttttacagag gaagagcttc tcgctatcga cgccatcgaa gcttcctaca 120
 atttctcccg ttcttcttct tcttcttctt ctgctgctcc gaccgtacaa gctacaacct 180
 ccgtccatgg ccacgaggag gatccaaatc aaatcccca taatatccgt cgccaattgc 240
 ctggttccat cacttcttct acatcttata aacgatttcc tctctcccg tgccgagcta 300
 ggaattttcc agcaatgagg tttggtggtt ggattttgta tagcaagact gctactgagg 360
 ttgataagcg agcaatgcag cttattaaag ttcttgatac caagagagat gaatctggaa 420
 tagcttttgt tggcttgat attgagtga gaccaagttt tagaaaaggt gttctcccg 480
 ggaagggtgc gactgtccag atatgtgtag atagtaatta ttgtgatgtt atgcatattt 540
 ttcattctgg tatccctcaa agtctccaac atcttattga agattcaaca cttgtaaagg 600
 taggtattgg aattgatggt gactctgtga agcttttcca tgactatgga gttagtatca 660
 aagatgttga ggatctttca gatttagcca accaaaaaat tgggtggagat aaaaaatggg 720
 gccttgccct actaactgag acacttggtt gcaaagagct cctgaagcca aacagaatca 780
 ggcttgggaa ctgggagttt tatcctctgt caaagcagca gttacaatac gcagcaacgg 840
 atgcttatgc ttcattggcat ctttacaagg ttcttaagga ctttctgat gctgtcagtg 900
 gctcataacg tgaaggagga agcttaaagg ttagcctata accccaagag ttagcatcaa 960
 atgatatgat acacctaata tagtcaagta gatgcaattc ttgtgaatat tgtatctagt 1020
 tctggtccct ttaaccgtcc agaaactag 1049

<210> 24
 <211> 288
 <212> PRT
 <213> Arabidopsis thaliana

<400> 24
 Met Ser Ser Ser Asn Trp Ile Asp Asp Ala Phe Thr Glu Glu Glu Leu
 1 5 10 15

Leu Ala Ile Asp Ala Ile Glu Ala Ser Tyr Asn Phe Ser Arg Ser Ser
 20 25 30

Ser Ser Ser Ser Ser Ala Ala Pro Thr Val Gln Ala Thr Thr Ser Val
 35 40 45

106290" 98T 96860

His	Gly	His	Glu	Glu	Asp	Pro	Asn	Gln	Ile	Pro	Asn	Asn	Ile	Arg	Arg		
50						55				60							
Gln	Leu	Pro	Arg	Ser	Ile	Thr	Ser	Ser	Thr	Ser	Tyr	Lys	Arg	Phe	Pro		
65					70					75					80		
Leu	Ser	Arg	Cys	Arg	Ala	Arg	Asn	Phe	Pro	Ala	Met	Arg	Phe	Gly	Gly		
			85						90					95			
Arg	Ile	Leu	Tyr	Ser	Lys	Thr	Ala	Thr	Glu	Val	Asp	Lys	Arg	Ala	Met		
		100						105					110				
Gln	Leu	Ile	Lys	Val	Leu	Asp	Thr	Lys	Arg	Asp	Glu	Ser	Gly	Ile	Ala		
		115					120					125					
Phe	Val	Gly	Leu	Asp	Ile	Glu	Trp	Arg	Pro	Ser	Phe	Arg	Lys	Gly	Val		
	130					135					140						
Leu	Pro	Gly	Lys	Val	Ala	Thr	Val	Gln	Ile	Cys	Val	Asp	Ser	Asn	Tyr		
145					150					155					160		
Cys	Asp	Val	Met	His	Ile	Phe	His	Ser	Gly	Ile	Pro	Gln	Ser	Leu	Gln		
				165					170					175			
His	Leu	Ile	Glu	Asp	Ser	Thr	Leu	Val	Lys	Val	Gly	Ile	Gly	Ile	Asp		
			180					185					190				
Gly	Asp	Ser	Val	Lys	Leu	Phe	His	Asp	Tyr	Gly	Val	Ser	Ile	Lys	Asp		
	195						200					205					
Val	Glu	Asp	Leu	Ser	Asp	Leu	Ala	Asn	Gln	Lys	Ile	Gly	Gly	Asp	Lys		
	210					215					220						
Lys	Trp	Gly	Leu	Ala	Ser	Leu	Thr	Glu	Thr	Leu	Val	Cys	Lys	Glu	Leu		
225					230					235					240		
Leu	Lys	Pro	Asn	Arg	Ile	Arg	Leu	Gly	Asn	Trp	Glu	Phe	Tyr	Pro	Leu		
				245					250					255			
Ser	Lys	Gln	Gln	Leu	Gln	Tyr	Ala	Ala	Thr	Asp	Ala	Tyr	Ala	Ser	Trp		
			260					265					270				
His	Leu	Tyr	Lys	Val	Leu	Lys	Asp	Leu	Pro	Asp	Ala	Val	Ser	Gly	Ser		
		275					280					285					

<210> 25
 <211> 22
 <212> DNA
 <213> Description of Artificial Sequence:
 Oligonucleotide

<400> 25
 ttcggaacca ccatcaaaca gg

<210> 26
 <211> 22
 <212> DNA
 <213> Description of Artificial Sequence:
 Oligonucleotide

<400> 26
 ttgctgcaac tctctcaggg cc 22

<210> 27
 <211> 21
 <212> DNA
 <213> Description of Artificial Sequence:
 Oligonucleotide

<400> 27
 tcagctgttg cccgtctcac t 21

<210> 28
 <211> 16
 <212> DNA
 <213> Description of Artificial Sequence:
 Oligonucleotide
 Other n=a, c, g, or t

<400> 28
 wgtgnagwan canaga 16

<210> 29
 <211> 27
 <212> DNA
 <213> Description of Artificial Sequence:
 Oligonucleotide

<400> 29
 gctccgcccataattcaa acaacac 27

<210> 30
 <211> 22
 <212> DNA
 <213> Description of Artificial Sequence:
 Oligonucleotide

<400> 30
 ttcgaaaaca ttacctccga tc 22

<210> 31
 <211> 25
 <212> DNA
 <213> Description of Artificial Sequence:
 Oligonucleotide

<400> 31
 ggcttttgca tttggtatct actag 25

<210> 32
<211> 25
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 32
atgtcatcgt caaattggat cgacg 25

<210> 33
<211> 27
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 33
cgcttatcaa cctcagtagc agtcttg 27

<210> 34
<211> 24
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 34
ttatgagcca ctgacagcat cagg 24

PB/5-31481A

1

3

4

28

09896186-062901